

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/422,548

TEAM 6

Eisenbach  
DATE: 07/11/95  
TIME: 09:23:37

INPUT SET: S4668 (from)

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Eaton, Dan L.  
6 DeSavage, Frederic J.  
7  
8 (ii) TITLE OF INVENTION: MPL LIGAND  
9  
10 (iii) NUMBER OF SEQUENCES: 32  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Genentech, Inc.  
14 (B) STREET: 460 Point San Bruno Blvd  
15 (C) CITY: South San Francisco  
16 (D) STATE: California  
17 (E) COUNTRY: USA  
18 (F) ZIP: 94080  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: patin (Genentech)  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER:  
28 (B) FILING DATE: 13-APR-1995  
29 (C) CLASSIFICATION:  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: 08/223263  
33 (B) FILING DATE: 04-APR-1994  
34  
35 (vii) PRIOR APPLICATION DATA:  
36 (A) APPLICATION NUMBER: 08/196689  
37 (B) FILING DATE: 15-FEB-1994  
38  
39 (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: 08/185607  
41 (B) FILING DATE: 21-JAN-1994  
42  
43 (vii) PRIOR APPLICATION DATA:  
44 (A) APPLICATION NUMBER: 08/176553  
45 (B) FILING DATE: 03-JAN-1994  
46

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INPUT SET: S4668.raw

47 (viii) ATTORNEY/AGENT INFORMATION:  
48 (A) NAME: Winter, Daryl B.  
49 (B) REGISTRATION NUMBER: 32,637  
50 (C) REFERENCE/DOCKET NUMBER: 871P3D1  
51  
52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: 415/225-1249  
54 (B) TELEFAX: 415/952-9881  
55 (C) TELEX: 910/371-7168  
56  
57 (2) INFORMATION FOR SEQ ID NO:1:  
58  
59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 353 amino acids  
61 (B) TYPE: amino acid  
62 (D) TOPOLOGY: linear  
63  
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
65  
66 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr  
67 1 5 10 15  
68  
69 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu  
70 20 25 30  
71  
72 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser  
73 35 40 45  
74  
75 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
76 50 55 60  
77  
78 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
79 65 70 75  
80  
81 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu  
82 80 85 90  
83  
84 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
85 95 100 105  
86  
87 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu  
88 110 115 120  
89  
90 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro  
91 125 130 135  
92  
93 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu  
94 140 145 150  
95  
96 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
97 155 160 165  
98  
99 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr

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	100	170	175	180
102	Ala Val Pro Ser	Arg Thr Ser Leu Val	Leu Thr Leu Asn Glu	Leu
103		185	190	195
105	Pro Asn Arg Thr	Ser Gly Leu Leu Glu	Thr Asn Phe Thr	Ala Ser
106		200	205	210
108	Ala Arg Thr Thr	Gly Ser Gly Leu Leu	Lys Trp Gln Gln Gly	Phe
109		215	220	225
111	Arg Ala Lys Ile	Pro Gly Leu Leu Asn	Gln Thr Ser Arg Ser	Leu
112		230	235	240
114	Asp Gln Ile Pro	Gly Tyr Leu Asn Arg	Ile His Glu Leu Leu	Asn
115		245	250	255
117	Gly Thr Arg Gly	Leu Phe Pro Gly Pro	Ser Arg Arg Thr	Leu Gly
118		260	265	270
120	Ala Pro Asp Ile	Ser Ser Gly Thr Ser	Asp Thr Gly Ser	Leu Pro
121		275	280	285
123	Pro Asn Leu Gln	Pro Gly Tyr Ser Pro	Ser Pro Thr His	Pro Pro
124		290	295	300
126	Thr Gly Gln Tyr	Thr Leu Phe Pro Leu	Pro Pro Thr Leu	Pro Thr
127		305	310	315
129	Pro Val Val Gln	Leu His Pro Leu Leu	Pro Asp Pro Ser	Ala Pro
130		320	325	330
132	Thr Pro Thr Pro	Thr Ser Pro Leu Leu	Asn Thr Ser Tyr	Thr His
133		335	340	345
135	Ser Gln Asn Leu	Ser Gln Glu Gly		
136		350	353	

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50  
CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCCTTG CCCGCCTTTG 100

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153  
154  
155 CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150  
156  
157  
158 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200  
159  
160  
161 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250  
162  
163  
164 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300  
165  
166  
167 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350  
168  
169  
170 AGACTGAGCC AGTGCCCAGA GGTTCACCCCT TTGCCTACAC CTGTCCTGCT 400  
171  
172  
173 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450  
174  
175  
176 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500  
177  
178  
179 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550  
180  
181  
182 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600  
183  
184  
185 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650  
186  
187  
188 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700  
189  
190  
191 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750  
192  
193  
194 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800  
195  
196  
197 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850  
198  
199  
200 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900  
201  
202  
203 TTCTTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950  
204  
205

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206 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACCTCGTG GACTCTTTCC 1000  
207  
208  
209 TGGACCCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050  
210  
211  
212 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100  
213  
214  
215 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150  
216  
217  
218 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200  
219  
220  
221 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250  
222  
223  
224 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300  
225  
226  
227 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350  
228  
229  
230 AACTGGACAA GATTTCTTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400  
231  
232  
233 GGGATACACA GGACTGAAAA GGAATCATT TTTCCTGTA CATTATAAAC 1450  
234  
235  
236 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500  
237  
238  
239 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550  
240  
241  
242 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600  
243  
244  
245 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650  
246  
247  
248 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCATCC CCTTTACTAT 1700  
249  
250  
251 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750  
252  
253  
254 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795  
255  
256  
257  
258 (2) INFORMATION FOR SEQ ID NO:3:

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/422,548**

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*INPUT SET: S4668.raw*

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Original Text